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APPLICANTS:

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SERIAL NO.:

09/647,978

FILED:

OCTOBER 6, 2000

FOR:

GENE ENCODING SYNTAXIN INTERACTING PROTEIN

SEQUENCE LISTING CERTIFICATION

I hereby certify that the paper copy of the Sequence Listing is identical to the computer readable copy of the Sequence Listing and that the Sequence Listing does not include matter which goes beyond the disclosure in the International Application as filed.

Date

Charles W. Ashbrook

Registration No. 27,610

WARNER-LAMBERT COMPANY

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<110> Warner-Lambert Company

<120> Gene Encoding Syntaxin Interacting Protein

<130> 09/647,978

<140> 09/647,978

<141> 2000-10-06

<150> PCT/US99/08568

<151> 1999-04-19

<150> 60/082,454

<151> 1998-04-20

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<170> PatentIn Ver. 2.1

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Ile His Glu Val Ile Pro Gly Gly Asp Cys Tyr Lys Asp Gly Arg Leu 50 60

Lys Pro Gly Asp Gln Leu Val Ser Ile Asn Lys Glu Ser Met Ile Gly 65 70 75 80

Val Ser Phe Glu Glu Ala Lys Ser Ile Ile Thr Arg Ala Lys Leu Arg
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Ser Glu Ser Pro Trp Glu Me Ala Phe Ile Arg Gln Lys Ser Tyr Cys
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Gly His Pro Gly Asn Ile Cys Cys Pro Ser Pro Gln Val Ser Glu Asp 115 120 125

Cys Gly Pro Gln Thr Ser Thr Phe Thr Leu Leu Ser Ser Pro Ser Glu
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Thr Leu Leu Pro Lys Thr Ser Ser Thr Pro Gln Thr Gln Asp Ser Thr 145 150 155 160

Phe Pro Ser Cys Lys Ala Ile Gln Thr Lys Pro Glu His Asp Lys Thr
165 170 175

Glu His Ser Pro Ile Thr Ser Leu Asp Asn Ser Pro Ala Asp Thr Ser Asn Ala Asp Ile Ala Pro Ala Trp Thr Asp Asp Asp Ser Gly Pro Gln Gly Lys Ile Ser Leu Asn Pro Ser Val Arg Leu Lys Ala glu Lys Leu Glu Met Ala Leu Asn Tyr Leu Gly Ile Gln Pro Thr Lys Glu Gln Arg Glu Ala Leu Arg Glu Gln Val Gln Ala Asp Ser/Lys Gly Thr Val Ser Phe Gly Asp Phe Val Gln Val Ala Arg Ser/Leu Phe Cys Leu Gln Leu Asp Glu Val Asn Val Gly Val His Glu /fle Pro Ser Ile Leu Asp Ser Gln Leu Pro Cys Asp Ser Leu Élu Ala Asp Glu Val Gly Lys Leu Arg Gln Glu Arg Asn Ala Ala Léu Glu Glu Arg Asn Val Leu Lys Glu Lys Leu Leu Glu Ser Glu Lys His Arg Lys Gln Leu Ile Glu Glu Leu Gln Asn Val Lys Gln Glp Ala Lys Ala Val Ala Glu Glu Thr Arg Ala Leu Arg Ser Arg Ile/His Leu Ala Glu Ala Ala Gln Arg Gln Ala His Gly Met Glu Met Asp Tyr Glu Glu Val Ile Arg Leu Leu Glu Ala Glu Val Ser Glu ∤eu Lys Ala Gln Leu Ala Asp Tyr Ser Asp Gln Asn Lys Glu Ser Val Gln Asp Leu Arg Lys Arg Val Thr Val Leu Asp Cys Gln

Leu Arg Lys Ser Glu Met Ala Arg Lys Ala Phe Lys Ala Ser Thr Glu

Arg Leu Leu Gly Phe Ile Glu Ala Ile Gln Glu Val Leu Leu Asp Sex 440 445 435 Ser Ala Pro Leu Ser Thr Leu Ser Glu Arg Arg Ala Val Leu A/a Ser 455 460 450 . Gln Thr Ser Leu Pro Leu Leu Ala Arg Asn Gly Arg Ser Phe Pro Ala 480 470 475 465 Thr Leu Leu Glu Ser Lys Glu Leu Val Arg Ser/Val Arg Ala Ile 485 490 Leu Asp Met Asp Cys Leu Pro Tyr Gly Trp Gly Glu Ala Tyr Thr Ala 500 505 Asp Gly Ile Lys Tyr Phe Ile Asn His Va/ Thr Gln Thr Thr Ser Trp 525 520 515 Ile His Pro Val Met Ser Ala Leu Asm Leu Ser Cys Ala Glu Glu Ser 540 535 Glu Glu Asp Cys Pro Arg Glu Ley Thr Asp Pro Lys Ser 545 550 555 <210> 3 <211> 2075 <212> DNA <213> Human <400> 3 cagcgcttgc agtcgggc/ta cggaggccgg gttgccagat tacgggaaag ccatttaaga 60 agttcctgga ataatat/tag tcagagtaat ataggatctg caggaagtgt ctcaagatag 120 ttggaaaaga agaat ttcta gactetteat caagatette atttatacag etgttaaate 180 caaggctact ttggt/gaaag catgaataaa aatacatcta ctgtagtatc acccagtcta 240 cttgaaaagg atcdtgcctt tcagatgatt acaattgcca aggaaacagg ccttggcctg 300 aaggtactag gaggaattaa ccggaatgaa ggcccattgg tatatattca ggaaattatt 360 cctggaggag agtgttataa ggatggtcgt ttgaagccag gagatcaact tgtctcagtc 420 aacaaggaat #tatgattgg tgtatcattt gaagaagcaa aaagcataat taccagagcc 480 aagttgaggt/tagaatctgc ttgggagata gcattcataa gacaaaaatc cgacaacatt 540 cagccagaa atctgtcatg tacatcactt atagaagctt caggagaata tggacctcaa 600 gcctcaacat taagtctttt ttcttctcct cctgaaatac taatcccaaa gacctcatcc 660

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35 40 45

Ile Gln Glu Ile Ile Pro Gly Gly Asp Cys Tyr Lys Asp Gly Arg Leu
50 55 60

Lys Pro Gly Asp Gln Leu Val Ser Val Asn Lys Glu Ser Met Ile Gly
65 70 75 80

Val Ser Phe Glu Glu Ala Lys Ser Ile Ile Thr Arg Ala Lys Leu Arg
85 90 95

Leu Glu Ser Ala Trp Glu Ile Ala Phe Ile Arg Gln Lys Ser Asp Asn 100 105 110

Ile Gln Pro Glu Asn Ley Ser Cys Thr Ser Leu Ile Glu Ala Ser Gly
115 120 125

Glu Tyr Gly Pro Gln/Ala Ser Thr Leu Ser Leu Phe Ser Ser Pro Pro 130 135 140

Glu Ile Leu Ile ro Lys Thr Ser Ser Thr Pro Lys Thr Asn Asn Asp 145 150 155 160

Ile Leu Ser Ser Cys Glu Ile Lys Thr Gly Tyr Asn Lys Thr Val Gln
165 170 175

Ile Pro Ile Thr Ser Glu Asn Ser Thr Val Gly Leu Ser Asn Thr Asp

OI

Val Ala Ser Ala Trp Thr Glu Asn Tyr Gly Leu Gln Glu Lys I e Ser 195 200 205

185

Leu Asn Pro Ser Val Arg Phe Lys Ala Glu Lys Leu Glu Met Ala Leu 210 215 220

Asn Tyr Leu Gly Ile Gln Pro Thr Lys Glu Gln His Gln Ala Leu Arg
225 230 235 240

Gln Gln Val Gln Ala Asp Ser Lys Gly Thr Val Ser Phe Gly Asp Phe
245 250 255

Val Gln Val Ala Arg Asn Leu Phe Cys Leu Gln Leu Asp Glu Val Asn 260 265 270

Val Gly Ala His Glu Ile Ser Asn Ile Leu Asp Ser Gln Leu Leu Pro 275 280 285

Cys Asp Ser Ser Glu Ala Asp Glu Met Glu Arg Leu Lys Cys Glu Arg 290 295 300

Asp Asp Ala Leu Lys Glu Val Asn Thr Leu Lys Glu Lys Leu Leu Glu 305 310 315 320

Ser Asp Lys Gln Arg Lys Gln Leu Thr Glu Glu Leu Gln Asn Val Lys 325 330 335

Gln Glu Ala Lys Ala Val Val Glu Glu Thr Arg Ala Leu Arg Ser Arg
340 345 350

Ile His Leu Ala Glu Ála Ala Gln Arg Gln Ala His Gly Met Glu Met 355 360 365

Asp Tyr Glu Glu Val Ile Arg Leu Leu Glu Ala Lys Ile Thr Glu Leu 370 375 380

Lys Ala Gln Ley Ala Asp Tyr Ser Asp Gln Asn Lys Glu Ser Val Gln 385 390 395 400

Asp Leu Lys Lys Arg Ile Met Val Leu Asp Cys Gln Leu Arg Lys Ser

Glu Met Ala Arg Lys Thr Phe Glu Ala Ser Thr Glu Lys Leu Leu His
420 425 430

Phe Va / Glu Ala Ile Gln Glu Val Phe Ser Asp Asn Ser Thr Pro Leu

435 440 445

Ser Asn Leu Ser Glu Arg Arg Ala Val Leu Ala Ser Gln Thr Sér Leu 450 455 460

Thr Pro Leu Gly Arg Asn Gly Arg Ser Ile Pro Ala Thr Leu Ala Leu 465 470 475 480

Glu Ser Lys Glu Leu Val Lys Ser Val Arg Ala Leu Zeu Asp Met Asp 485 490 495

Cys Leu Pro Tyr Gly Trp Glu Glu Ala Tyr Thr Ala Asp Gly Ile Lys 500 505 510

Tyr Phe Ile Asn His Val Thr Gln Thr Thr Ser Trp Ile His Pro Val 515 520 525

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